

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=5; day=4; hr=15; min=49; sec=41; ms=312;]

=====

Application No: 10577893 Version No: 2.0

Input Set:**Output Set:**

Started: 2011-04-27 17:46:59.122
Finished: 2011-04-27 17:47:01.361
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 239 ms
Total Warnings: 28
Total Errors: 0
No. of SeqIDs Defined: 28
Actual SeqID Count: 28

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-04-27 17:46:59.122
Finished: 2011-04-27 17:47:01.361
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 239 ms
Total Warnings: 28
Total Errors: 0
No. of SeqIDs Defined: 28
Actual SeqID Count: 28

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Ludmerer, Steven W.
 Graham, Donald J.
 LaFemina, Robert L.
 Flores, Osvaldo A.
 Pizzuti, Maura
 Traboni, Cinzia

<120> HCV REPLICONS CONTAINING NS5B FROM
 GENOTYPE 2B

<130> 21564YP

<140> 10577893
 <141> 2011-04-27

<150> PCT/US2004/036575
 <151> 2004-11-03

<150> 60/517,605
 <151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HCV

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa = threonine or serine

<221> VARIANT
 <222> (24)...(24)
 <223> Xaa = asparagine or serine

<221> VARIANT
 <222> (31)...(31)
 <223> Xaa = methionine or isoleucine

<221> VARIANT
 <222> (392)...(392)
 <223> Xaa = isoleucine or leucine

<400> 1
 Ser Met Ser Tyr Xaa Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly Pro
 1 5 10 15
 Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg

	20							25					30				
Phe	His	Asn	Lys	Val	Tyr	Ser	Thr	Thr	Ser	Arg	Ser	Ala	Ser	Leu	Arg		
		35					40					45					
Ala	Lys	Lys	Val	Thr	Phe	Asp	Arg	Val	Gln	Val	Leu	Asp	Ala	His	Tyr		
		50					55					60					
Asp	Ser	Val	Leu	Gln	Asp	Val	Lys	Arg	Ala	Ala	Ser	Lys	Val	Ser	Ala		
65			70					75					80				
Arg	Leu	Leu	Thr	Val	Glu	Glu	Ala	Cys	Ala	Leu	Thr	Pro	Pro	His	Ser		
		85					90					95					
Ala	Lys	Ser	Arg	Tyr	Gly	Phe	Gly	Ala	Lys	Glu	Val	Arg	Ser	Leu	Ser		
		100					105					110					
Arg	Arg	Ala	Val	Asn	His	Ile	Arg	Ser	Val	Trp	Glu	Asp	Leu	Leu	Glu		
		115					120					125					
Asp	Gln	His	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	Val		
		130					135					140					
Phe	Cys	Ile	Asp	Pro	Thr	Lys	Gly	Gly	Lys	Lys	Pro	Ala	Arg	Leu	Ile		
145			150					155					160				
Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	Tyr		
		165					170					175					
Asp	Ile	Ala	Gln	Lys	Leu	Pro	Lys	Ala	Ile	Met	Gly	Pro	Ser	Tyr	Gly		
		180					185					190					
Phe	Gln	Tyr	Ser	Pro	Ala	Glu	Arg	Val	Asp	Phe	Leu	Leu	Lys	Ala	Trp		
		195					200					205					
Gly	Ser	Lys	Lys	Asp	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	Phe		
		210					215					220					
Asp	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	Tyr		
225			230					235					240				
Gln	Ala	Cys	Ser	Leu	Pro	Gln	Glu	Ala	Arg	Thr	Val	Ile	His	Ser	Leu		
		245					250					255					
Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Thr	Asn	Ser	Lys	Gly	Gln		
		260					265					270					
Ser	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser		
		275					280					285					
Met	Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile	Lys	Ala	Leu	Ala	Ala	Cys	Lys		
		290					295					300					
Ala	Ala	Gly	Ile	Val	Asp	Pro	Val	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu		
305			310					315					320				
Val	Val	Ile	Ser	Glu	Ser	Gln	Gly	Asn	Glu	Glu	Asp	Glu	Arg	Asn	Leu		
		325					330					335					
Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	Asp		
		340					345					350					
Leu	Pro	Arg	Pro	Glu	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	Ser		
		355					360					365					
Asn	Val	Ser	Val	Ala	Leu	Asp	Ser	Arg	Gly	Arg	Arg	Arg	Tyr	Phe	Leu		
		370					375					380					
Thr	Arg	Asp	Pro	Thr	Thr	Pro	Xaa	Thr	Arg	Ala	Ala	Trp	Glu	Thr	Val		
385			390					395					400				
Arg	His	Ser	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Gln	Tyr	Ala		
		405					410					415					
Pro	Thr	Ile	Trp	Val	Arg	Met	Val	Ile	Met	Thr	His	Phe	Phe	Ser	Ile		
		420					425										

Glu	Leu	Ser	Arg	Val	Ala	Ala	Thr	Leu	Arg	Lys	Leu	Gly	Ala	Pro	Pro
				485						490				495	
Leu	Arg	Ala	Trp	Lys	Ser	Arg	Ala	Arg	Ala	Val	Arg	Ala	Ser	Leu	Ile
			500					505					510		
Ala	Gln	Gly	Ala	Arg	Ala	Ala	Ile	Cys	Gly	Arg	Tyr	Leu	Phe	Asn	Trp
		515					520					525			
Ala	Val	Lys	Thr	Lys	Leu	Lys	Leu	Thr	Pro	Leu	Pro	Glu	Ala	Ser	Arg
	530					535					540				
Leu	Asp	Leu	Ser	Gly	Trp	Phe	Thr	Val	Gly	Ala	Gly	Gly	Gly	Asp	Ile
545					550				555					560	
Tyr	His	Ser	Val	Ser	His	Ala	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Cys	Leu
			565					570						575	
Leu	Leu	Leu	Ser	Val	Gly	Val	Gly	Ile	Phe	Leu	Leu	Pro	Asp	Arg	
			580				585						590		

<210> 2

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> HCV

<221> variation

<222> (3)...(3)

<223> n = A or T

<221> variation

<222> (9)...(9)

<223> n = C or A

<221> variation

<222> (13)...(13)

<223> n = A or T

<221> variation

<222> (15)...(15)

<223> n = A or C

<221> variation

<222> (21)...(21)

<223> n = A or G

<221> variation

<222> (24)...(24)

<223> n = C or G

<221> variation

<222> (28)...(28)

<223> n = T or C

<221> modified_base

<222> (30)...(30)

<223> n = G or C

<221> variation

<222> (33)...(33)

<223> n = C or A

<221> variation

<222> (71)...(71)

<223> n = A or G

<221> variation

<222> (93)...(93)

<223> n = G or T

<221> variation

<222> (1174)...(1174)

<223> n = A or C

<400> 2

```
tcnatgtcnt acnnttggac nggngccntn atnacacccat gtggggcccgag agaggagaag 60
ttaccgatca nccctctgag taattcgctc atncgggttcc ataataagggt gtactccaca 120
acctcgagga gtgcctctct gagggcaaaag aagggtgactt ttgacagggt gcagggtgctg 180
gacgcacact atgactcagt cttgcaggac gttaagcggg ccgcctctaa ggtagtgctg 240
aggctcctca cggtagagga agcctgcgcg ctgaccccgcc cccactccgc caaatcgcg 300
tacggatttg gggcaaaaga ggtgcgcagc ttatctagga gggccgttaa ccacatccgg 360
tccgtgtggg aggacctcct ggaagaccaa cataccccaa ttgacacaa tatcatggct 420
aaaaatgagg tgttctgcat tgatccaact aaagggtggga aaaagccagc tcgcctcatc 480
gtataccccc accttgggggt cagggtgtgc gaaaagatgg ccctctatga catcgacaaa 540
aagcttccca aagcgataat gggggccatcc tatgggttcc aatactctcc cgcagaacgg 600
gtcgatttcc tcctcaaagc ttggggaagt aagaaggacc caatgggggt ctcgatgac 660
acccgctgct ttgactcaac cgtcacggag agggacataa gaacagaaga atccatatat 720
caggcttggt ctctgcctca agaagccaga actgtcatac actcgctcac tgagagactt 780
tacgtaggag ggcccatgac aaacagcaaa gggcaatcct gcggctacag gcgttgccgc 840
gcaagcggtg ttttcaccac cagcatgggg aataccatga catgttacat caaagccctt 900
gcagcgtgta aggctgcagg gatcgtggac cctgttatgt tgggtgtgtg agacgacctg 960
gtcgtcatct cagagagcca aggtaacgag gaggacgagc gaaacctgag agctttcacg 1020
gaggctatga ccagggtattc cgccccctcc ggtgaccttc ccagaccgga atatgacttg 1080
gagcttataa catcctgctc ctcaaacgta tcggtagcgc tggactctcg gggtcgcccgc 1140
cgggtacttcc taaccagaga ccctaccact ccantcaccc gagctgcttg ggaaacagta 1200
agacactccc ctgtcaattc ttggctgggc aacatcatcc agtacgcccc cacaatctgg 1260
gtccggatgg tcataatgac tcacttcttc tccatactat tggcccagga cactctgaac 1320
caaaatctca attttgagat gtacggggca gtatactcgg tcaatccatt agacctaccg 1380
gccataattg aaaggctaca tgggcttgaa gccttttcac tgcacacata ctctccccac 1440
gaactctcac ggggtggcagc aactctcaga aaacttggag cgctccccct tagagcgtgg 1500
aagagtcggg cgcggtgccgt gagagcttca ctcatcgccc aaggagcgag ggcggccatt 1560
tgtggccgct acctcttcaa ctgggcggtg aaaacaaagc tcaaactcac tccattgccc 1620
gaggcgagcc gcctggattt atccgggtgg ttcaccgtgg gcgcggcgcg gggcgacatt 1680
tatcacagcg tgtcgcatgc ccgaccccgcc ctattactcc tttgcctact cctacttagc 1740
gtaggagtag gcatcttttt actccccgat cgatga 1776
```

<210> 3

<211> 1394

<212> PRT

<213> Artificial Sequence

<220>

<223> HCV

<221> VARIANT

<222> (1215)...(1215)

<223> Xaa = asparagine or serine

<221> VARIANT

<222> (904)...(904)

<223> Xaa = valine or alanine

<400> 3

Met	Ala	Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly
1				5					10					15	
Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly
			20					25					30		
Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys
		35					40					45			
Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr
	50					55				60					
Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp
65					70					75					80
Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr
				85					90					95	
Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala
				100				105						110	
Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu
	115						120					125			
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu
	130					135					140				
Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys
145					150					155					160
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met
				165					170					175	
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro
			180					185					190		
Ala	Val	Pro	Gln	Thr	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly
	195						200					205			
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr
	210					215					220				
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly
225					230					235					240
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly
				245					250					255	
Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly
		260					265						270		
Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile
	275					280					285				
Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile
	290					295					300				
Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val
305					310					315					320
Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn
				325					330					335	
Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly
		340						345					350		
Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe
	355						360					365			
Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly
	370					375					380				
Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val
385					390					395					400

Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	405	410	415
Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	420	425	430
Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	435	440	445
Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	450	455	460
Arg	Thr	Gly	Arg	Gly	Arg	Met	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	465	470	475
Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	485	490	495
Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	500	505	510
Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	515	520	525
His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	530	535	540
Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	545	550	555
Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	565	570	575
Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	580	585	590
Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	595	600	605
Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	610	615	620
Ser	Ala	Asp	Leu	Glu	Val	Val	Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	625	630	635
Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Thr	Gly	Ser	Val	Val	645	650	655
Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Ile	Val	Pro	Asp	660	665	670
Arg	Glu	Phe	Leu	Tyr	Gln	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	675	680	685
His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys	690	695	700
Gln	Lys	Ala	Leu	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	705	710	715
Ala	Ala	Pro	Val	Val	Glu	Ser	Lys	Trp	Arg	Ala	Leu	Glu	Thr	Phe	Trp	725	730	735
Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	740	745	750
Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe	755	760	765
Thr	Ala	Ser	Ile	Thr	Ser	Pro	Leu	Thr	Thr	Gln	Ser	Thr	Leu	Leu	Phe	770	775	780
Asn	Ile	Leu	Gly	Gly	Trp	Val	Ala	Ala	Gln	Leu	Ala	Pro	Pro	Ser	Ala	785	790	795
Ala	Ser	Ala	Phe	Val	Gly	Ala	Gly	Ile	Ala	Gly	Ala	Ala	Val	Gly	Ser	805	810	815
Ile	Gly	Leu	Gly	Lys	Val	Leu	Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	820	825	830
Gly	Val	Ala	Gly	Ala	Leu	Val	Ala	Phe	Lys	Val	Met	Ser	Gly	Glu	Met	835	840	845
Pro	Ser	Thr	Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro			

850		855		860
Gly Ala Leu Val Val	Gly Val Val Cys Ala Ala Ile Leu Arg Arg His			
865	870	875		880
Val Gly Pro Gly Glu	Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala			
	885	890		895
Phe Ala Ser Arg Gly Asn His Xaa Ser Pro Thr His Tyr Val Pro Glu				
900	905			910
Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile				
915	920			925
Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser				
930	935			940
Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys				
945	950			955
Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro				
	965			970
				975
Gln Leu Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly				
980	985			990
Val Trp Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala				
995	1000			1005
Gln Ile Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro				
1010	1015			1020
Lys Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr				
1025	1030			1035
Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala				
	1045			1050
				1055
Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly				
1060	1065			1070
Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro				
1075	1080			1085
Cys Gln Val Pro Ala				